

REMARKS

Favorable reconsideration, reexamination, and allowance of the present patent application are respectfully requested in view of the foregoing amendments and the following remarks. The foregoing amendments do not add new matter and are fully supported by the originally filed claims, page 8, lines 20-24, page 15, lines 8-20, page 16, lines 13-23, page 17, lines 1-6, page 18, lines 10-15.

Objection to the Specification

At page 2 of the Office Action, the disclosure as a whole was objected to because it allegedly contains an embedded hyperlink and/or other form of browser-executable code. Applicant respectfully requests reconsideration of this objection.

The specification has been amended to remove portions of the embedded hyperlink in each instance, so that it is no longer browser-executable.

For at least the foregoing reasons, Applicant respectfully submits that the disclosure as a whole is not objectionable, and therefore respectfully requests withdrawal of the objection thereto.

Rejection under 35 U.S.C. § 112, second paragraph

In the Office Action, beginning at page 2, Claims 1-10 were rejected under 35 U.S.C. § 112, second paragraph, as reciting subject matters that allegedly are indefinite, more specifically in the recitation of “an ArcA protein does not normally function”, and “wherein the ArcA protein that normally functions is a protein”. Applicant respectfully requests reconsideration of this rejection.

The claims have been amended to recite “the production of ArcA protein is reduced or eliminated” and have further clarified the antecedent phrases. This amendment is based on the description at page 15, lines 16-18 of the specification. Applicants assert that the claims are definite and clear in its meaning and intent.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-10 fully comply with 35 U.S.C. § 112, second paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

In the Office Action, beginning at page 3, Claim 6 was further rejected under 35

U.S.C. § 112, second paragraph, as reciting subject matters that allegedly are indefinite. Applicant respectfully requests reconsideration of this rejection. Claim 6 was further rejected as being allegedly vague and indefinite in the recitation of “DNA hybridizable with the nucleotide sequence of nucleotide numbers 101 to 817 of SEQ ID NO: 31...”. Claim 6 has been amended by deletion of the allegedly indefinite phrases and insertion of the specific stringent conditions, and therefore, applicants assert this claim is definite and clear in its intent and meaning.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-10 fully comply with 35 U.S.C. § 112, second paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

Rejection under 35 U.S.C. § 112, first paragraph

In the Office Action, beginning at page 4, Claims 1-6 and 8-10 were rejected under 35 U.S.C. § 112, first paragraph, as reciting subject matters that allegedly fail to comply with the written description requirement. Applicant respectfully requests reconsideration of this rejection.

Attached as Exhibit A are alignments of ArcA protein *E. coli* with that of the other γ -proteobacteria. This data clearly demonstrates that the amino acid sequence of ArcA protein is highly conserved among γ -proteobacteria. As such, a person skilled in the art can obtain the homologous arcA gene from γ -proteobacterium other than *E. coli* and *Pantoea ananatis* based on the disclosed nucleotide sequence of arcA gene of *E. coli* (SEQ ID NO: 31) or *Pantoea ananatis* (SEQ ID NO:19), and use the obtained arcA gene to disrupt a chromosomal arcA gene in each γ -proteobacterium. Applicants assert the description of SEQ ID NO:31 and SEQ ID NO:19 are sufficient to describe the genus of ArcA genes/proteins from other γ -proteobacterium, as one of skill in the art would be able to ascertain other species and their respective ArcA gene/protein sequences. Therefore, these two exemplified and described sequences constitute a representative number of species since the relevant structural properties are easily ascertained and determined due to the highly homologous nature of the ArcA genes/proteins among γ -proteobacterium.

Similarly, applicants assert that the description of *E.coli* and *Pantoea ananatis*

which have been modified so that an ArcA protein does not function normally are sufficient to adequately describe the genus of γ -proteobacterium encompassed by the claims. Specifically, as shown in the attached Exhibit A, the common feature of this genus of bacteria is their structural commonality of having a disrupted ArcA gene/protein. This common structural feature is present in any species of the genus, and is therefore sufficient to demonstrate possession of the genus of γ -proteobacterium.

For at least the foregoing reasons, Applicant respectfully submits that Claims 1-6 and 8-10 fully comply with 35 U.S.C. § 112, first paragraph, and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 112.

Rejection under 35 U.S.C. § 102(b)

In the Office Action, beginning at page 6, Claims 1-9 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Cotter et al. Applicant respectfully requests reconsideration of this rejection.

Claim 1 relates to a γ -proteobacterium including, *inter alia*, “a target substance synthesized via TCA cycle” and “as compared to a wild-type γ -proteobacterium”. Support for the subject matter in claim 1 can be found, e.g., at page 8, lines 23-24, and page 17, lines 4-6. Although Cotter et al. discloses arcA gene-disrupted strains, the strains described by Cotter et al. do not have an ability to produce a target substance synthesized via the tricarboxylic acid cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via the tricarboxylic acid cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant strain as described in page 9, lines 23-24 of the specification, and the MG1655 Δ sucA strain in which sucA gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-9 are not anticipated by Cotter et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 7, Claims 1-10 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Iuchi et al. Applicant respectfully requests reconsideration of this rejection.

As stated above, the claims recite “a target substance synthesized via TCA cycle” and “as compared to a wild-type γ -proteobacterium”. Although Iuchi et al. discloses *arcA* gene-disrupted strains, the strains disclosed by Iuchi et al. do not have an ability to produce a target substance synthesized via TCA cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via TCA cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant strain as described in page 9, lines 23-24 of the English specification, and the MG1655 Δ *sucA* strain in which *sucA* gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the English specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-10 are not anticipated by Iuchi et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 6, Claims 1-10 were rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Nystrom et al. Applicant respectfully requests reconsideration of this rejection.

Similar to our arguments presented above, the claims recite “a target substance synthesized via TCA cycle” and “as compared to a wild-type γ -proteobacterium”. Although Nystrom et al. discloses *arcA* gene-disrupted strains, Nystrom et al. does not disclose strains which have have an ability to produce a target substance synthesized via TCA cycle in an amount more than an amount of the substance produced by a wild-type bacterium. In contrast, the strains used in the Examples of the present specification are strains modified to have an ability to produce a target substance synthesized via TCA cycle. That is, the WC196 strain disclosed in Example 2 is an L-lysine-producing mutant

strain as described in page 9, lines 23-24 of the English specification, and the MG1655Δ sucA strain in which sucA gene is disrupted is an L-glutamic acid-producing strain, as described in page 11, lines 5-9 of the English specification.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claims 1-10 are not anticipated by Nystrom et al., are therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

In the Office Action, beginning at page 8, Claim 2 was rejected under 35 U.S.C. § 102(b), as reciting subject matters that allegedly are anticipated by Sugimoto et al.. Applicants note that the patent number listed on page 8 of the office action is incorrect. The correct patent number, which is listed correctly on the PTO-892, is 5,919,694. Applicant respectfully requests reconsideration of this rejection.

Claim 2 has been amended to limit the number of amino acid substitutions, deletions or insertions to “up to 10”. Therefore, this limitation clearly removes the disclosure of Sugimoto et al. as prior art.

For at least the foregoing reasons, Applicant respectfully submits that the subject matters of Claim 2 is not anticipated by Sugimoto et al., is therefore not unpatentable under 35 U.S.C. § 102(b), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(b).

Rejection under 35 U.S.C. § 102(e)

In the Office Action, beginning at page 9, Claims 1-10 were rejected under 35 U.S.C. § 102(e), as reciting subject matters that allegedly are anticipated by Cervin et al. Applicant respectfully requests reconsideration of this rejection.

Applicants hereby submit a translation of the priority documents and a verification by the translator, as Exhibit B. These documents are sufficient to effectively remove Cervin et al. as prior art since the priority date of July 12, 2002 can be relied upon by applicants, because the priority documents provide support for the claimed subject matter.

For at least the foregoing reasons, Applicant respectfully submits that the subject

matters of Claims 1-10 are not anticipated by Cervin et al., because Cervin et al. is not prior art to the claimed subject matter and therefore the claims are not unpatentable under 35 U.S.C. § 102(e), and therefore respectfully requests withdrawal of the rejection thereof under 35 U.S.C. § 102(e).


Conclusion

For at least the foregoing reasons, Applicant respectfully submits that the present patent application is in condition for allowance. An early indication of the allowability of the present patent application is therefore respectfully solicited.

If Examiner Vogel believes that a telephone conference with the undersigned would expedite passage of the present patent application to issue, she is invited to call on the number below.

It is not believed that extensions of time are required, beyond those that may otherwise be provided for in accompanying documents. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and the undersigned respectfully authorizes that our deposit account 50-3077 be charged any required fees.

Respectfully submitted,

By: _____

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Date: June 10, 2005

EXHIBIT A

ALIGNMENT DATA

In the alignment data, each accession number means the following species of γ -proteobacterium.

S4704	<i>Shigella flexneri</i> _2457T
SF4433	<i>Shigella flexneri</i>
C5488	<i>E. coli</i> _CFT073
ECs5359	<i>E. coli</i> _O157J
Z6004	<i>E. coli</i> _O157
JW4364	<i>E. coli</i> _J
B4401	<i>E. coli</i>
STM4598	<i>Salmonella typhimurium</i>
SC4443	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Choleraesuis</i>
T4637	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhi</i> Ty2
STY4947	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhi</i>
SPA4408	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Paratyphi</i>
YPTB0601	<i>Yersinia pseudotuberculosis</i>
YP3725	<i>Yersinia pestis</i> biovar <i>Medievalis</i>
Y3721	<i>Yersinia pestis</i> KIM
YP00458	<i>Yersinia pestis</i>
ECA3893	<i>Erwinia carotovora</i>
Plu0562	<i>Photobacterium luminescens</i>
VC2368	<i>Vibrio cholerae</i>
VP0489	<i>Vibrio parahaemolyticus</i>
PBPRA0547	<i>Photobacterium profundum</i>
VF2120	<i>Vibrio fischeri</i>
VV0646	<i>Vibrio vulnificus</i> YJ016
VV10548	<i>Vibrio vulnificus</i>
PM0219	<i>Pasteurella multocida</i>
SO3988	<i>Shewanella oneidensis</i>
MS1504	<i>Mannheimia succiniciproducens</i>
HD0278	<i>Haemophilus ducreyi</i>
HI0884	<i>Haemophilus influenzae</i>
VF1570	<i>Vibrio fischeri</i>

BLASTP 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= eco:b4401 arcA, dye, fexA, msp, seg, sfrA, cpxC: negative response regulator of genes in aerobic pathways, (sensors, ArcB and CpxA) (A)
(238 letters)

Database: GENES+DGENES: GENES+DGENES(amino acid sequence)
1,405,264 sequences; 537,705,622 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E Value
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Top 10 Select operation

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<input checked="" type="checkbox"/> sfl:SF4433 arcA: negative response regulator of genes in aerobic...	478	e-134
<input checked="" type="checkbox"/> ecc:c5488 arcA: aerobic respiration control protein arcA [KO:K02...	478	e-134
<input checked="" type="checkbox"/> ecs:ECs5359 negative response regulator of genes in aerobic path...	478	e-134
<input checked="" type="checkbox"/> ece:Z6004 arcA: negative response regulator of genes in aerobic ...	478	e-134
<input checked="" type="checkbox"/> ecj:JW4364 arcA: Aerobic respiration control protein ArcA (Dye r...	478	e-134
<input checked="" type="checkbox"/> eco:b4401 arcA, dye, fexA, msp, seg, sfrA, cpxC: negative respon...	478	e-134
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<input checked="" type="checkbox"/> sec:SC4443 arcA: response regulator (OmpR family) in two-compone...	477	e-134
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<input type="checkbox"/> sty:STY4947 arcA: global response regulator [KO:K02483]	477	e-134
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<input type="checkbox"/> ypk:y3721 arcA: negative response regulator of genes in aerobic ...	445	e-124
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<input type="checkbox"/> eca:ECA3893 arcA, cpxC, dye, fexA, msp, sfrA: aerobic respiratio...	445	e-124
<input type="checkbox"/> plu:plu0562 arcA: negative response regulator of genes in aerobi...	442	e-123
<input type="checkbox"/> vch:VC2368 fexA: aerobic respiration control protein FexA [KO:KO...	427	e-119
<input type="checkbox"/> vpa:VP0489 fexA: aerobic respiration control protein FexA [KO:KO...	417	e-116
<input type="checkbox"/> ppr:PBPA0547 fexA: putative aerobic respiration control protein...	412	e-114
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<input type="checkbox"/> vvv:VV0646 fexA: aerobic respiration control protein FexA [KO:KO...	411	e-114
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<input type="checkbox"/> son:S03988 arcA: aerobic respiratiqn control protein ArcA [KO:KO...	392	e-108
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<input type="checkbox"/> hdu:HD0278 arcA: aerobic respiration control protein ArcA [KO:KO...	377	e-103
<input type="checkbox"/> hin:HI0884 arcA: aerobic respiration control protein arcA homolo...	374	e-103
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>sfx:S4704 arcA; negative response regulator of genes in aerobic pathways
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Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

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Sbjct: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180

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>sfl:SF4433 arcA; negative response regulator of genes in aerobic pathways
(sensors, ArcB and CpxA) [KO:K02483]
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Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

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>ecc:c5488 arcA; aerobic respiration control protein arcA [KO:K02483]
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Identities = 238/238 (100%), Positives = 238/238 (100%)

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>ecs:ECs5359 negative response regulator of genes in aerobic pathways ArcA
[K0:K02483]
Length = 238

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Identities = 238/238 (100%), Positives = 238/238 (100%)

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>ece:Z6004 arcA; negative response regulator of genes in aerobic pathways.
(sensors, ArcB and CpxA) [K0:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

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Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
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Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ
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Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLED 238
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>ecj:JW4364 arcA; Aerobic respiration control protein ArcA (Dye resistance
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Identities = 238/238 (100%), Positives = 238/238 (100%)

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Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
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Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238
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Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238

>eco:b4401 arcA, dye, fexA, msp, seg, sfrA, cpxC; negative response regulator
of genes in aerobic pathways, (sensors, ArcB and CpxA)
[KO:K02483]
Length = 238

Score = 478 bits (1230), Expect = e-134
Identities = 238/238 (100%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238
SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIIATIHGEGYRFGDLED
Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIIATIHGEGYRFGDLED 238

>stm:STM4598 arcA; response regulator (OmpR family) in two-component regulatory
system with ArcB (or CpxA), regulates genes in aerobic
pathways [KO:K02483]
Length = 238

Score = 477 bits (1227), Expect = e-134
Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ
 Sbjct: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL 238
 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL+D
 Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLQD 238

>sec:SG4443 arcA: response regulator (OmpR family) in two-component regulatory
 system with ArcB (or CpxA), regulates genes in aerobic
 pathways
 Length = 238

Score = 477 bits (1227), Expect = e-134
 Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
 Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR
 Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ
 Sbjct: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL 238
 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL+D
 Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLQD 238

>stt:t4637 arcA: global response regulator [KO:K02483]
 Length = 238

Score = 477 bits (1227), Expect = e-134
 Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
 Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR
 Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ
 Sbjct: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL 238
 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDL+D
 Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLQD 238

>sty:STY4947 arcA: global response regulator [KO:K02483]
 Length = 238

Score = 477 bits (1227), Expect = e-134

Identities = 237/238 (99%), Positives = 238/238 (100%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIATIHGEGYRFCGDL 238
SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIATIHGEGYRFCGDL+D
Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIATIHGEGYRFCGDLQD 238

>spt:SPA4408 arcA: global response regulator [K0:K02483]
Length = 238

Score = 474 bits (1219), Expect = e-133
Identities = 236/238 (99%), Positives = 237/238 (99%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIATIHGEGYRFCGDL 238
SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIATIHGEGYRFCGDL+D
Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRIRKHFESTPDTPEIATIHGEGYRFCGDLQD 238

>yps:YPTB0601 arcA: response regulator (OmpR family), in two-component regulatory
system with ArcB (or CpxA), regulates genes in aerobic
respiration [K0:K02483]
Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDELVTRNTLKSIFEAGY V+EA DGAEMH ILSE DINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAGYVVEANDGAEMHHILSENDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
TMNL +V EERR VESYKFNWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLSSVGEERRLVESYKFNWELDINSRSLVSPTGEHYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLED 238
SR ELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLE+
Sbjct: 181 SRGELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLEE 238

>ypm:YP3725 arcA; aerobic respiration control protein [K0:K02483]
Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE+VTRNTLKSIFEAGY V+EA DGAEMH ILSE DINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAGYVVYEANDGAEMHHILSENDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
TMNL +V EERR VESYKFNWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLSSVGEERRLVESYKFNWELDINSRSLVSPTGEHYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLED 238
SR ELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLE+
Sbjct: 181 SRGELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLEE 238

>ypk:y3721 arcA; negative response regulator of genes in aerobic pathways,
sensors, ArcB and CpxA [K0:K02483]
Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE+VTRNTLKSIFEAGY V+EA DGAEMH ILSE DINLVIMDINLPGK
Sbjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAGYVVYEANDGAEMHHILSENDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR
Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
TMNL +V EERR VESYKFNWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGKIQ
Sbjct: 121 TMNLSSVGEERRLVESYKFNWELDINSRSLVSPTGEHYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLED 238
SR ELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLE+
Sbjct: 181 SRGELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLEE 238

>ype:YP00458 arcA, dye, fexA, sfrA, seg, msp, cpxC; aerobic respiration control
protein [K0:K02483]
Length = 238

Score = 445 bits (1145), Expect = e-124
Identities = 221/238 (92%), Positives = 227/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE+VTRNTLKSIFEAGY V+EA DGAEMH ILSE DINLVIMDINLPGK

Sbjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAEGYVVYEANDGAEMHHILSENDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR 120
 NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR

Sbjct: 61 NGLLLARELREQASVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 TMNL +V EERR VESYKFNWELDINSRSL+ P GE YKLPRSEFRAMLHFCENPGKIQ

Sbjct: 121 TMNLSSVGEERRLVESYKFNWELDINSRSLVSPTGEHYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLED 238
 SR ELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLE+

Sbjct: 181 SRGELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLEE 238

>eca:ECA3893 arcA, cpxC, dye, fexA, msp, sfrA; aerobic respiration control
 protein [KO:K02483]
 Length = 238

Score = 445 bits (1144), Expect = e-124
 Identities = 224/238 (94%), Positives = 228/238 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
 MQTPHILIVEDELVTRNTLKSIFEAEGY V EATDGAEMH ILSE DINLVIMDINLPGK

Sbjct: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYVHEATDGAEMHHILSENDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR 120
 NGLLLARELREQA VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR

Sbjct: 61 NGLLLARELREQATVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 TMNLG+ +EERR VESY+FNWELDINSRSLI P GEQYKLPRSEFRAMLHFCENPGKIQ

Sbjct: 121 TMNLGSGTEERRLVESYRFNWELDINSRSLISPAGEQYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLED 238
 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFEST DTPEIIATIHGEGYRFGDLE+

Sbjct: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTADTPEIIATIHGEGYRFGDLEN 238

>plu:plu0562 arcA; negative response regulator of genes in aerobic pathways,
 (sensors, ArcB and CpxA) (dye resistance protein)
 [KO:K02483]
 Length = 238

Score = 442 bits (1138), Expect = e-123
 Identities = 221/237 (93%), Positives = 226/237 (95%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
 MQTPHILIVEDE+VTRNTLKSIFEAEGY V+EATDG+EMH ILS DINLVIMDINLPGK

Sbjct: 1 MQTPHILIVEDEIVTRNTLKSIFEAEGYIVYEATDGSEMHHILSNNNDINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR 120
 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR

Sbjct: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNNLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 TMNL VSEERR VESYKFNWELDINSRSLI P GE YKLPRSEFRAMLHFCENPGKIQ

Sbjct: 121 TMNLNVSEERRQVESYKFNWELDINSRSLISPAGEPYKLPRSEFRAMLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLE 237
 +RA+LLKKMTGRELKPHDRTVDVTIRRIKHFESTPDT EIIATIHGEGYRFGDLE

Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTMEIIATIHGEGYRFGDLE 237

>vch:VC2368 fexA: aerobic respiration control protein FexA [K0:K02483]
Length = 238

Score = 427 bits (1098), Expect = e-119
Identities = 210/238 (88%), Positives = 223/238 (93%)

Query: 1 MQTPHILIVEDELVTRNTLKSI FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTP ILIVEDE VTRNTLKSI FEAEGY VFEA++G EMHQ+LS+Y INLVIMDINLPGK
Sbjct: 1 MQTPQILIVEDEQVTRNTLKSI FEAEGYAVFEASNGEEMHQVLSDYPI NLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLP RSEFRAMLHFCENPGKIQ 180
+M+ GT EE+RSVE Y FNGWELDI NSRSL+ PDG+ YKLP RSEFRA+LHFCENPGKIQ
Sbjct: 121 SMHAGTTQEEKRSVEKYFNGWELDI NSRSLVSPDGDSYKLP RSEFRALLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRI RKFHESPTDPEI IATIHGEGYRFGCDLED 238
+RA+LLKKMTGRELKPHDRTVDVTIRRI RKFES TPEI IATIHGEGYRFGCDLED
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRI RKFESVSGTPEI IATIHGEGYRFGCDLED 238

>vpa:VP0489 fexA: aerobic respiration control protein FexA [K0:K02483]
Length = 238

Score = 417 bits (1073), Expect = e-116
Identities = 206/238 (86%), Positives = 219/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKSI FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTP ILIVEDE VTRNTLKSI FEAEGY VFEA+DG EMHQ+LS+ INLVIMDINLPGK
Sbjct: 1 MQTPQILIVEDEQVTRNTLKSI FEAEGYAVFEASDGEEMHQVLSDNSINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGLLLARELREQAN+ALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR
Sbjct: 61 NGLLLARELREQANIALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLP RSEFRAMLHFCENPGKIQ 180
+M+ V EE+RSVE Y+FNGW LDINSRSL+ P G+ YKLP RSEFRA+LHFCENPGKIQ
Sbjct: 121 SMSTNAVQEEKRSVEKYFNGWLDINSRSLVSPAGDSYKLP RSEFRALLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRI RKFHESPTDPEI IATIHGEGYRFGCDLED 238
+RA+LLKKMTG ELKPHDRTVDVTIRRI RKFES TPEI IATIHGEGYRFGCDLED
Sbjct: 181 TRADLLKKMTGGELKPHDRTVDVTIRRI RKFESVSGTPEI IATIHGEGYRFGCDLED 238

>ppr:PBPR0547 fexA: putative aerobic respiration control protein FexA [K0:K02483]
Length = 239

Score = 412 bits (1060), Expect = e-114
Identities = 199/238 (83%), Positives = 220/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKSI FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTPHILIVEDE VTRNTLKSI FEAEGY VFEA DGAEMHQ+LSE+ ++LVIMDINLPGK
Sbjct: 1 MQTPHILIVEDEHVTRNTLKSI FEAEGYTVFEANDGAEMHQLSEHPVHLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGLLLARELREQ ++ALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLL+R
Sbjct: 61 NGLLLARELREQDMALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLP RSEFRAMLHFCENPGKIQ 180
MN G +E+++ VE Y+FNGW L+INSRSL+ P G+Q+KLPRSEFRA+LHFCENPGKIQ
Sbjct: 121 AMNOGLPTEDKKLVERYEFNGWSLEINSRSLVSPSGDQFKLP RSEFRALLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRI RKFESTPDTPEIIATIHGEGYRFGDLED 238
+R +LLKKMTGRELKPHDRTVDVTIRRI RKFES DTPEI+ATIHGEGYRFGDL +
Sbjct: 181 TRGDLLKKMTGRELKPHDRTVDVTIRRI RKFESVADTPEIVATIHGEGYRFGDLNE 238

>vfi:VF2120 arcA: aerobic respiration control protein ArcA [K0:K02483]
Length = 239

Score = 411 bits (1056), Expect = e-114
Identities = 200/238 (84%), Positives = 220/238 (92%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTP ILIVEDE VTRNTLKSIFEAEGY+VFEA+DG EMH++LSE +NLVIMDINLPGK
Sbjct: 1 MQTPQILIVEDEHVTNTLKSIFEAEGYNVFEASDGEEMHKVLEQQNLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGLLLARELRE+ ++ALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLL+R
Sbjct: 61 NGLLLARELRERGD MALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLP RSEFRAMLHFCENPGKIQ 180
+MN TV E+++ VE Y FNGW ++INSRSL+ P GE YKLPRSEFRA+LHFCENPGKIQ
Sbjct: 121 SMNQNTVVEDKKMVERYVFNWTV EINSRSLVSPSGESYKLP RSEFRALLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRI RKFESTPDTPEIIATIHGEGYRFGDLED 238
+RA+LLKKMTGRELKPHDRTVDVTIRRI RKFES DTPEIIATIHGEGYRFGDLE+
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRI RKFESVDTPEIIATIHGEGYRFGDLEE 238

>vvy:VV0646 fexA: aerobic respiration control protein FexA [K0:K02483]
Length = 238

Score = 411 bits (1056), Expect = e-114
Identities = 205/237 (86%), Positives = 218/237 (91%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
MQTP ILIVEDE VTRNTLKSIFEAEGY VFEA++G EMH +LSE INLVIMDINLPGK
Sbjct: 1 MQTPQILIVEDEQVTRNTLKSIFEAEGYAVFEASNGDEMHHMLSENSINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR
Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDI NSRSLIGPDGEQYKLP RSEFRAMLHFCENPGKIQ 180
+M+ + EE+RSVE Y+FNGW LDINSRSLI P G+ YKLPRSEFRA+LHFCENPGKIQ
Sbjct: 121 SMSSSVMPEEKRSVEKYEFNGWVLDINSRSLISPSGDGYKLP RSEFRALLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRI RKFESTPDTPEIIATIHGEGYRFGDLE 237
+RA+LLKKMTGRELKPHDRTVDVTIRRI RKFES TPEIIATIHGEGYRFGDLE
Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRI RKFESVSGTPEIIATIHGEGYRFGDLE 237

>vvu:VV10548 fexA: aerobic respiration control protein FexA [K0:K02483]
Length = 238

Score = 411 bits (1056), Expect = e-114
Identities = 205/237 (86%), Positives = 218/237 (91%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
 MQTP ILIVEDE VTRNTLKSIFEAEGY VFEA++G EMH +LSE INLVIMDINLPGK
 Sbjct: 1 MQTPQILIVEDEQVTRNTLKSIFEAEGYAVFEASNGDEMHHLSSENSINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120
 NGLLLARELREQA+VALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR
 Sbjct: 61 NGLLLARELREQADVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 +M+ + EE+RSVE Y+FNGW LDINSRSLI P G+ YKLPRSEFRA+LHFCENPGKIQ
 Sbjct: 121 SMSSSVMPEEKRSVEKYEFNGWVLDINSRSLISPSGDGYKLPRSEFRALLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLE 237
 +RA+LLKKMTGRELKPHDRTVDVTIRRIKHFES TPEIIATIHGEGYRFCGDLE
 Sbjct: 181 TRADLLKKMTGRELKPHDRTVDVTIRRIKHFESVSGTPEIIATIHGEGYRFCGDLE 237

>pmu:PM0219 arcA: aerobic respiration control protein [KO:K02483]
 Length = 236

Score = 394 bits (1011), Expect = e-108
 Identities = 194/237 (81%), Positives = 210/237 (88%), Gaps = 1/237 (0%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
 M TP ILIVEDE +TRNTLKSIFEAEGY+VFEA DGA+MH+ILS INLVIMDINLPGK
 Sbjct: 1 MGTPQILIVEDEAITRNTLKSIFEAEGYEVFEAADGAQMHRILSNKVINLVIMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120
 NGL+LARELRE N ALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLL R
 Sbjct: 61 NGLMLARELRETTNTALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLQR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 TM + + +E Y+FNGW LD+NSR+LI P+GE+YKLPRSEFRAMLHFCENPGKIQ
 Sbjct: 121 TMOENS-KDSHPIEQYRFNGWTLDLNSRTLINPEGEYKLPRSEFRAMLHFCENPGKIQ 179

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLE 237
 +R ELLKKMTGRELKP DRTVDVTIRRIKHFES P+TPEIIATIHGEGYRFCG+LE
 Sbjct: 180 TREELLKKMTGRELKPDRTVDVTIRRIKHFEDHPETPEIIATIHGEGYRFCGELE 236

>son:S03988 arcA: aerobic respiration control protein ArcA [KO:K02483]
 Length = 238

Score = 392 bits (1006), Expect = e-108
 Identities = 194/238 (81%), Positives = 209/238 (87%)

Query: 1 MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLPGK 60
 MQ PHILIVEDE VTRNTL+SIFEAEGY V EA DGAEMH+ + E INLV+MDINLPGK
 Sbjct: 1 MQNPHILIVEDEAVTRNTLSIFEAEGYVTEANDGAEMHKAMQENKINLVVMDINLPGK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLSR 120
 NGLLLARELRE N+ L+FLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLL+R
 Sbjct: 61 NGLLLARELREINNIGLIFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIARNLLTR 120

Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 + G EE+ SVE Y+FN W L+INSRSL+ P GE YKLPRSEFRAMLHF ENPGKI
 Sbjct: 121 VNSAGNEVEEKSSVEYYRFNDWSLEINSRSLVSPQGESYKLPRSEFRAMLHFVENPGKIL 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFCGDLED 238
 +RA+LL KMTGRELKPHDRTVDVTIRRIKHFES PDTPEIIATIHGEGYRFCG+LED
 Sbjct: 181 TRADLLMKMTGRELKPHDRTVDVTIRRIKHFESLPDTPEIIATIHGEGYRFCGNLED 238

>msu:MS1504 ompR: response regulators consisting of a CheY-like receiver domain
and a HTH DNA-binding domain [K0:K02483].
Length = 236

Score = 382 bits (982), Expect = e-105
Identities = 190/240 (79%), Positives = 209/240 (87%), Gaps = 7/240 (2%)

Query: 1 MQTPHILIVEDELVTRNTLKSI FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLP GK 60
M +P ILIVEDE VTRNTLKSI FEAEGY+VFEATDG +MHQI+ +INLV+MDINLP GK
Sbjct: 1 MLSPQILIVEDET VTRNTLKSI FEAEGYEVFEATDGNQMHQIIETQEI NLVVM DINLP GK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGL+LARELRE+ N ALMFLTGRDNEVDKILGLEIGADDYITKPFNPREL I RARNLL R
Sbjct: 61 NGLMLARELREKNTALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELA I RARNLLHR 120

Query: 121 TMNLGTVSEERRS—VESYKFNWEL DINSRSLIGPDGEQYKLP RSEFRAMLHFCENPG 177
TM E+ S V++Y+FNGW LDIN R+LI P+ +YKLP RSEFRAMLHFCENPG
Sbjct: 121 TM—AENEKSNTHVDAYRFNGW TLDINKRALIDPESVEYKLP RSEFRAMLHFCENPG 176

Query: 178 KIQSRAELLKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLE 237
KIQ+R +LLKKMTGRELKP DRTVDVTIRRIRKHF E PDTPEIIATIHGEGYRFG++E
Sbjct: 177 KIQTRELLKKMTGRELKPDRTVDVTIRRIRKHFEDHPDTPEIIATIHGEGYRFGGEIE 236

>hdu:HD0278 arcA: aerobic respiration control protein Arca [K0:K02483]
Length = 237

Score = 377 bits (968), Expect = e-103
Identities = 188/237 (79%), Positives = 204/237 (86%)

Query: 1 MQTPHILIVEDELVTRNTLKSI FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLP GK 60
MQ P ILIVEDELVTRNTLKSI FEAEGY+VFEA+DG EM+ IL++ INLVIMDINLP GK
Sbjct: 1 MQNPQILIVEDELVTRNTLKSI FEAEGYEVFEASDGTEMNT ILAQQTINLVIMDINLP GK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGL+LARELRE +ALMFLTGRDNEVDKILGLE+GADDYITKPFNPRELTI RARNLL R
Sbjct: 61 NGLMLARELRENTKMALMFLTGRDNEVDKILGLEVGADDYITKPFNPRELTI RARNLLHR 120

Query: 121 TMNLGTVSEERRSVESYKFNWEL DINSRSLIGPDGEQYKLP RSEFRAMLHFCENPGKIQ 180
TM ESY+FNGW LD+NSRSLI P+GE KLP RSEFRA+LHFCENPGKIQ
Sbjct: 121 TMLEKDKVSHSEQESYRFNGW TLDVNSRSLI TPEGEINKLP RSEFRALLHFCENPGKIQ 180

Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIRKHFESTPDTPEIIATIHGEGYRFGDLE 237
+R +LL KMTGRELKPHDRTVDVTIRRIRKHF E +TPEII TIHGEGYRFGC +E
Sbjct: 181 TREDLLLKMTGRELKPHDRTVDVTIRRIRKHFEDHLNTPEIIVTIHGEGYRFGQIE 237

>hin:HI0884 arcA: aerobic respiration control protein arca homolog [K0:K02483]
Length = 236

Score = 374 bits (960), Expect = e-103
Identities = 183/237 (77%), Positives = 206/237 (86%), Gaps = 1/237 (0%)

Query: 1 MQTPHILIVEDELVTRNTLKSI FEAEGYDVFEATDGAEMHQILSEYDINLVIMDINLP GK 60
M TP IL+VEDE+VTRNTLK I FEAEGYDVFEA +G EMH IL+ ++INLV+MDINLP GK
Sbjct: 1 MTTPKILVVEDEIVTRNTLKG I FEAEGYDVFEAENGVEMHILANHNINLVVM DINLP GK 60

Query: 61 NGLLLARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSR 120
NGLLLARELRE+ ++ L+FLTGRDNEVDKILGLEIGADDY+TKPFNPRELTI RARNLL R

Sbjct: 61 NGLLLARELREELSPLIFLTGRDNEVDKILGLEIGADDYLT KPFNPRELTI RARNLLHR 120
 Query: 121 TMNLGTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQ 180
 M E E Y+FNW+LD+NS SLI P+G+++KLPRSEFRAMLHFCENPGK+Q
 Sbjct: 121 AMP-HQEKENTFGREFYRFGWKLDLNSHSLITPEGQEFKLPRSEFRAMLHFCENPGKLQ 179
 Query: 181 SRAELLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGDLE 237
 +R ELLKKMTGRELKP DRTVDVTIRRIKHF P+TP II TIHGEGYRFGD+E
 Sbjct: 180 TREELLKKMTGRELKPDRTVDVTIRRIKHFEDHPNTPNIIMTIHGEGYRFGDIE 236

>vfi:VF1570 torR: TorCAD operon transcriptional regulatory protein TorR
 [KO:K02483]
 Length = 232

Score = 217 bits (552), Expect = 2e-55
 Identities = 110/231 (47%), Positives = 152/231 (65%), Gaps = 2/231 (0%)

Query: 5 HILIVEDELVTRNTLKSIFEAGYDVFEATDGAEMHQILSEYDINLVIMDINLPGKNGLL 64
 HIL+VEDE+VTR+ L FEAGY V EA GAEM IL+E ++L+++DINLPG++GLL
 Sbjct: 4 HILVVEDEVVTRSKLVGYFEAGYQVSEATGAEMRSILAEQKVDLIMLDINLPGEDGLL 63
 Query: 65 LARELREQANVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTI RARNLLSRTMNL 124
 LARELR Q+N+ ++ +TGR + +D+I+GLE+GADDY+TKP REL +R +NL R M+L
 Sbjct: 64 LARELRSQSNIGIILVTGRTDSIDRIVGLEMGADDYVTKPVELRELLVRVKNLFWR-MSL 122
 Query: 125 GTVSEERRSVESYKFNWELDINSRSLIGPDGEQYKLPRSEFRAMLHFCENPGKIQSRAE 184
 E +F W DI R+L +GE KL ++E+ ++ P + SR
 Sbjct: 123 ANEPVELDESNNVRFGEWTFDIQRRAL-SNNGEPVKLTAEYELLVALSSYPNTVLSRER 181
 Query: 185 LLKKMTGRELKPHDRTVDVTIRRIKHFESTPDTPEIIATIHGEGYRFGD 235
 +L ++ R P+DRT+DV IRR+R E P P+I T+HGEGY F GD
 Sbjct: 182 ILNMI SHRVDAPNDRTIDVLI RRMRAKMEVDPKNPQIFVTVHGEGYMFAGD 232

Database: GENES+DGENES: GENES+DGENES(amino acid sequence)
 Posted date: Jun 6, 2005 5:28 AM
 Number of letters in database: 319,922,540
 Number of sequences in database: 911,393

Database: dgenes
 Posted date: Jun 4, 2005 8:12 AM
 Number of letters in database: 217,783,082
 Number of sequences in database: 493,871

Lambda	K	H
0.319	0.138	0.396

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 249,767,882
 Number of Sequences: 1405264
 Number of extensions: 9983109
 Number of successful extensions: 34529
 Number of sequences better than 10.0: 30
 Number of HSP's better than 10.0 without gapping: 3346
 Number of HSP's successfully gapped in prelim test: 1949
 Number of HSP's that attempted gapping in prelim test: 26334

Number of HSP's gapped (non-prelim): 5566
length of query: 238
length of database: 537,705,622
effective HSP length: 121
effective length of query: 117
effective length of database: 367,668,678
effective search space: 43017235326
effective search space used: 43017235326
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 72 (32.3 bits)